



**University of
Zurich**^{UZH}

**Zurich Open Repository and
Archive**

University of Zurich
University Library
Strickhofstrasse 39
CH-8057 Zurich
www.zora.uzh.ch

Year: 2015

Revisiting susceptibility testing in MDR-TB by a standardized quantitative phenotypic assessment in a European multicentre study

Cambau, E ; Viveiros, M ; Machado, D ; Raskine, L ; Ritter, C ; Tortoli, E ; Matthys, V ; Hoffner, S ; Richter, E ; Perez Del Molino, M L ; Cirillo, D M ; van Soolingen, D ; Böttger, E C

Abstract: **OBJECTIVES:** Treatment outcome of MDR-TB is critically dependent on the proper use of second-line drugs as per the result of in vitro drug susceptibility testing (DST). We aimed to establish a standardized DST procedure based on quantitative determination of drug resistance and compared the results with those of genotypes associated with drug resistance. **METHODS:** The protocol, based on MGIT 960 and the TB eXiST software, was evaluated in nine European reference laboratories. Resistance detection at a screening drug concentration was followed by determination of resistance levels and estimation of the resistance proportion. Mutations in 14 gene regions were investigated using established techniques. **RESULTS:** A total of 139 *Mycobacterium tuberculosis* isolates from patients with MDR-TB and resistance beyond MDR-TB were tested for 13 antituberculous drugs: isoniazid, rifampicin, rifabutin, ethambutol, pyrazinamide, streptomycin, para-aminosalicylic acid, ethionamide, amikacin, capreomycin, ofloxacin, moxifloxacin and linezolid. Concordance between phenotypic and genotypic resistance was >80%, except for ethambutol. Time to results was short (median 10 days). High-level resistance, which precludes the therapeutic use of an antituberculous drug, was observed in 49% of the isolates. The finding of a low or intermediate resistance level in 16% and 35% of the isolates, respectively, may help in designing an efficient personalized regimen for the treatment of MDR-TB patients. **CONCLUSIONS:** The automated DST procedure permits accurate and rapid quantitative resistance profiling of first- and second-line antituberculous drugs. Prospective validation is warranted to determine the impact on patient care.

DOI: <https://doi.org/10.1093/jac/dku438>

Posted at the Zurich Open Repository and Archive, University of Zurich

ZORA URL: <https://doi.org/10.5167/uzh-111176>

Journal Article

Published Version

Originally published at:

Cambau, E; Viveiros, M; Machado, D; Raskine, L; Ritter, C; Tortoli, E; Matthys, V; Hoffner, S; Richter, E; Perez Del Molino, M L; Cirillo, D M; van Soolingen, D; Böttger, E C (2015). Revisiting susceptibility testing in MDR-TB by a standardized quantitative phenotypic assessment in a European multicentre study. *Journal of Antimicrobial Chemotherapy*, 70(3):686-696.

DOI: <https://doi.org/10.1093/jac/dku438>

Revisiting susceptibility testing in MDR-TB by a standardized quantitative phenotypic assessment in a European multicentre study

E. Cambau^{1*}, M. Viveiros², D. Machado², L. Raskine¹, C. Ritter³, E. Tortoli⁴, V. Matthys⁵, S. Hoffner⁶, E. Richter⁷, M. L. Perez Del Molino⁸, D. M. Cirillo⁴, D. van Soolingen^{9,10} and E. C. Böttger^{3†}

¹AP-HP, Hôpital Lariboisière, Service de Bactériologie, Centre National de Référence des Mycobactéries et de la Résistance des Mycobactéries aux Antituberculeux; IAME UMR1137, INSERM, Université Paris Diderot, 75010 Paris, France; ²Grupo de Micobactérias, Unidade de Microbiologia Médica, Instituto de Higiene e Medicina Tropical, Universidade Nova de Lisboa (IHMT/UNL), Rua da Junqueira 100, 1349-008 Lisboa, Portugal; ³Institut für Medizinische Mikrobiologie, Nationales Zentrum für Mykobakterien, Universität Zürich, Zürich, Switzerland; ⁴IRCCS San Raffaele Scientific Institute, Emerging Bacterial Pathogens Unit Supranational Reference Laboratory, via Olgettina 60, 20132 Milan, Italy; ⁵National Reference Centre of Tuberculosis and Mycobacteria, Communicable and Infectious Diseases, Scientific Institute of Public Health (WIV-ISP), Brussels, Belgium; ⁶Department of Microbiology, Public Health Agency of Sweden and Department of Microbiology, Cell and Tumor Biology, Karolinska Institute, Stockholm, Sweden; ⁷National Reference Center for Mycobacteria, Forschungszentrum Borstel, Borstel, Germany; ⁸Servicio de Microbiología, CH Universitario de Santiago, Centro de Referencia de Micobacterias de Galicia, Choupana S/N, 15705 Santiago de Compostela, Spain; ⁹Tuberculosis Reference Laboratory, National Institute for Public Health and the Environment (RIVM), PO Box 1, 3720 BA Bilthoven, The Netherlands; ¹⁰Department of Pulmonary Diseases/Department of Clinical Microbiology, Radboud University Medical Centre, PO Box 9101, Nijmegen, The Netherlands

*Corresponding author. Service de Bactériologie-Virologie, Groupe Hospitalier Lariboisière-Fernand Widal, AP-HP, Paris, France.
Tel: +33-1-49-95-65-51; Fax: +33-1-49-95-85-37; E-mail: emmanuelle.cambau@lrp.ap-hop-paris.fr
†E. Cambau, M. Viveiros, D. Machado, L. Raskine, C. Ritter, D. van Soolingen and E. C. Böttger belong to ESGMYC (ESCMID Study Group for Mycobacterial Infections).

Received 19 July 2014; returned 9 September 2014; revised 27 September 2014; accepted 8 October 2014

Objectives: Treatment outcome of MDR-TB is critically dependent on the proper use of second-line drugs as per the result of *in vitro* drug susceptibility testing (DST). We aimed to establish a standardized DST procedure based on quantitative determination of drug resistance and compared the results with those of genotypes associated with drug resistance.

Methods: The protocol, based on MGIT 960 and the TB eXiST software, was evaluated in nine European reference laboratories. Resistance detection at a screening drug concentration was followed by determination of resistance levels and estimation of the resistance proportion. Mutations in 14 gene regions were investigated using established techniques.

Results: A total of 139 *Mycobacterium tuberculosis* isolates from patients with MDR-TB and resistance beyond MDR-TB were tested for 13 antituberculous drugs: isoniazid, rifampicin, rifabutin, ethambutol, pyrazinamide, streptomycin, *para*-aminosalicylic acid, ethionamide, amikacin, capreomycin, ofloxacin, moxifloxacin and linezolid. Concordance between phenotypic and genotypic resistance was >80%, except for ethambutol. Time to results was short (median 10 days). High-level resistance, which precludes the therapeutic use of an antituberculous drug, was observed in 49% of the isolates. The finding of a low or intermediate resistance level in 16% and 35% of the isolates, respectively, may help in designing an efficient personalized regimen for the treatment of MDR-TB patients.

Conclusions: The automated DST procedure permits accurate and rapid quantitative resistance profiling of first- and second-line antituberculous drugs. Prospective validation is warranted to determine the impact on patient care.

Keywords: antibiotic susceptibility testing, DST, antituberculous drugs, TB eXiST, MGIT

Introduction

MDR-TB is a major problem in the global fight against TB.^{1–3} MDR-TB is defined as resistance to at least isoniazid and rifampicin, the two cornerstones of the standard short-course chemotherapy.^{4,5} Consequently, treatment of MDR-TB requires the use of second-line drugs such as fluoroquinolones and aminoglycosides.^{6–8} Moreover, the treatment of XDR-TB, i.e. MDR-TB with additional resistance to fluoroquinolones and to amikacin, capreomycin or kanamycin, requires a hand-tailored regimen using the few remaining active drugs.

The treatment regimen for MDR- and XDR-TB is designed according to the results of drug susceptibility testing (DST), to ensure that the patient receives at least four drugs to which the *Mycobacterium tuberculosis* strain is susceptible.^{6–8} Since administration of appropriate therapy is a major prognostic factor, accurate testing of second-line drugs is mandatory.^{6,7,9–12} However, this testing is generally poorly standardized and often not quality controlled, which increases the risk of providing inadequate treatment.^{13–16}

Several techniques, based on critical proportion and critical concentration, have been described for *M. tuberculosis* DST.^{8,9,17–19} Procedures for determining isoniazid and rifampicin resistance are standardized and quality controlled, allowing for relatively accurate determination of resistance rates for MDR-TB surveillance at national and supranational levels.^{2,3,14,15,20,21} However, for second-line drugs these procedures are in part unreliable.^{13,15,22} In addition to poor reproducibility and extended laboratory turnaround times, currently established techniques provide no information on quantitative levels of drug resistance, limiting the possibility of individualized treatment.

Commercially available molecular tests have been recently implemented to detect mutations associated with resistance, especially to isoniazid and rifampicin.²³ In addition, reference laboratories use more extended sequencing of molecular targets to trace mutations associated with resistance.^{24,25}

Mycobacterial growth indicator tube (MGIT) DST is a well-established, standardized, semi-automated liquid system that provides reproducible results for first-line antituberculous drugs on the basis of critical concentration testing using the Becton-Dickinson (BD) MGIT 960 instrumentation (BD, Sparks, MD, USA).²⁶ The suitability of the system for second-line DST has also been evaluated.²⁷ The TB eXiST (extended individual susceptibility testing) software (BD) for interpretation of DST on the basis of the MGIT instrumentation was developed to allow for continuous growth monitoring and more detailed analysis.²⁸ Here, we used the MGIT 960 instrumentation equipped with the TB eXiST software to establish quantitative DST for *M. tuberculosis*. The procedure was designed to combine the endpoints of proportion and concentration testing with continuous monitoring of bacterial growth. We validated the specificity of the resistance detected by assessing the concordance with genetic profiles of resistance. Quantitative DST provides results on quantitative measures of resistance, which can help in optimizing treatment regimens for MDR-TB patients.

Materials and methods

TB eXiST susceptibility testing protocol

The following antituberculous agents were tested: isoniazid, ethionamide, rifampicin, rifabutin, ethambutol, streptomycin, *para*-aminosalicylic

acid, pyrazinamide, ofloxacin, moxifloxacin, amikacin, capreomycin and linezolid. Antituberculous drugs were purchased from Sigma (St Louis, MO, USA), except for pyrazinamide, linezolid and moxifloxacin, which were provided by BD, Pfizer (Singapore) and Merck (Whitehouse Station, NJ, USA), respectively. The drug concentrations selected for testing (Table 1) were based on literature data on drug resistance, distribution of the WT isolates [epidemiological cut-off (ECOFF)], critical concentrations and *in vivo* drug concentrations.^{29–31} Stock solutions were prepared in-house according to the manufacturers' recommendations. A 10× solution was prepared in a volume of 200 µL and added to a 7 mL MGIT tube along with 0.8 mL of OADC (BD). The 100% inoculum for MGIT testing was prepared as follows. Briefly, strains were grown for an additional 2 days after MGIT reached positivity (growth units >400) and used as pure inoculum or strains were grown until 5 days after positivity and diluted to 1:5 in 7H9 supplemented with 10% OADC. After 10- and 100-fold dilutions in MGIT medium, 0.5 mL of the 100%, 10% and 1% inocula were distributed into the growth control tubes. The 1% inoculum was termed the growth control (GC). An equal volume of 0.5 mL of the 100% inoculum was distributed in all the drug-containing tubes.

Strains were submitted to a screening protocol in order to distinguish WT strains from strains suspected of resistance. This protocol consisted of testing all drugs at the lowest drug concentration (Table 1) used as a screening concentration, which corresponds to an optimized critical or ECOFF concentration. Strains were submitted to a quantitative testing protocol for those drugs for which they were suspected to be resistant on the basis of screening concentration testing. For quantitative testing, three to four concentrations per drug were used, except for pyrazinamide where only one concentration was tested (Table 1).

MDR-TB cases and participating centres

Patients living in a European country at the time of diagnosis, whatever their country of birth, were included if their *M. tuberculosis* strain was MDR. Each centre included between 10 and 30 randomly chosen MDR cases diagnosed in 2009; however, if there were <10 cases, cases from 2010 were also included (Table S1, available as Supplementary data at JAC Online). Clinical *M. tuberculosis* strains were subjected to resistome analysis, i.e. a search for resistance-associated gene mutations by using commercial line probe assays followed by PCR sequencing when necessary. The gene regions studied are listed in Table 2.

Expert laboratories from nine European countries (Belgium, France, Germany, Italy, the Netherlands, Portugal, Spain, Sweden and Switzerland) participated in the study. This protocol received agreement from the institutional ethics review boards of each centre. At least one representative of each centre participated at the meetings organized: (i) at the beginning of the study to agree on the protocol; (ii) following the calibration and proficiency testing to optimize the protocol; and (iii) several times during the study, i.e. when phenotypic (culture-based) and genotypic (gene mutation-based) results became available. Each centre followed its established procedures for quality assurance. A steering committee (E. C., M. V. and E. C. B.) met several times between the group meetings and analysed the data. The interlaboratory reproducibility of the protocol was assessed by comparing results obtained in each of the participant laboratories for a set of 10 *M. tuberculosis* control strains: 5 strains for calibration (strain susceptibility was known to the participant) and 5 strains for evaluating the proficiency testing (strain susceptibility was unknown to the participant). These strains were provided by the National Center for Mycobacteria, Institute of Medical Microbiology, University of Zurich. In addition, each centre tested three to five WT pan-susceptible clinical strains isolated in their country. The calibration panel included three strains monoresistant to isoniazid (two with a *katG* S315T mutation and one with an *inhA* c–15t mutation conferring resistance also to ethionamide), one strain resistant to isoniazid (*katG* S315T) and streptomycin (*rrs* a523g), and one strain resistant to rifampicin and rifabutin

(*rpoB* H526Y). The proficiency testing included two strains with resistance to isoniazid (one *inhA* c-15t and one *katG* S315T), one strain resistant to rifampicin and rifabutin (*rpoB* S531L), one strain resistant to isoniazid (*katG* S315T) and to streptomycin (*rpsL* K43R), and one strain resistant to isoniazid (*katG* S315T) and to ethambutol (*embB* M306V).

Results

General features of TB eXiST DST

Drug resistance was initially detected by testing growth at the screening drug concentration. Resistance was subsequently quantified using higher drug concentrations. Since TB eXiST results are available in real time, the growth was recorded in parallel in control tubes and in drug-containing tubes. Figure 1 shows examples of growth curves for the three control tubes that contained 100%, 10% and 1% of the inoculum, resulting in three parallel curves separated by a theoretical mean of 3.5 days, which is the approximate time for an *M. tuberculosis* bacterial population to multiply by 10-fold. When growth was observed in the drug-containing tube before the GC (1% inoculum) was positive, this indicated that >1% of the population was growing in the presence of the drug, i.e. as per proportion testing the strain is considered resistant at the corresponding drug concentration. By studying bacterial growth at several drug concentrations, we observed that the quantitative levels of resistance differed significantly for the different antituberculous drugs and strains studied (Figure 1).

The time to result, calculated as the time elapsed until the GC became positive, was <30 days in all centres. Statistics, calculated in three of the nine centres, showed mean and median values of time to results between 10 and 11 days with a range of 8–30 days. For most isolates, the time to positivity in the drug-containing tubes was shorter than that of the GC and equal to that of the 100% inoculum, since for most strains and drugs the resistant proportion was close to 100%. The mean and median time to obtain resistance testing results was calculated as 4 and 5 days (range 3.5–13.5 days). Since growth curves were observed in a real-time manner, resistance could be suspected as rapidly as 5 days after inoculation (Figure 1b and c).

All laboratories performed the calibration and proficiency testing. A high rate of concordance (88%–97% with regard to strain and drug) was observed. Adjustments were necessary for the preparation of the stock solutions and we compared the results of quantitative resistance with regard to strains with the same genotype. This led to the exclusion of some of the data, for which we suspected a problem of drug preparation: rifabutin (19 results were excluded), *para*-aminosalicylic acid (15 results were excluded) and ethionamide (15 results were excluded).

Assessment of resistance for clinical strains

Testing growth at the screening concentration, i.e. the lowest drug concentration, distinguished susceptible strains from resistant strains (Table 1). Among the 139 MDR strains studied, resistance to fluoroquinolones and to amikacin or capreomycin was observed for 10 strains, corresponding to an XDR rate of 7.2%. Resistant strains were submitted to quantitative testing for confirmation of resistance by retesting at the screening drug concentration and for quantitative determination of the level of

resistance by studying growth at two to three additional higher drug concentrations, except for pyrazinamide for which we tested only a single concentration. The resistance patterns are presented in Table 1.

All strains studied were MDR strains; however, various levels of resistance were observed for isoniazid and rifampicin. For isoniazid, four levels of resistance were observed: low-level resistance with growth at 0.1 mg/L, but no growth at 1 mg/L (11 strains); two intermediate levels of resistance with growth at 0.1 and 1 mg/L, but no growth at 3 and 10 mg/L (51 strains) or growth at 0.1, 1 and 3 mg/L, but no growth at 10 mg/L (58 strains); and high-level resistance with growth at all drug concentrations (19 strains). For rifampicin, the resistance was high level for 84% of the strains. Cross-resistance to rifabutin was observed for 98% of the strains, although the levels of resistance were different for the two rifamycins.

In total, 720 resistant characters were observed, with a resistant character being defined as one drug resistance observed in one isolate. Low-level resistance, i.e. resistance to the screening concentration, but susceptibility at higher drug concentrations, was observed in 16% of the test results and at varying rates according to the drug, from 5% (rifampicin) to 73% (ethambutol). Conversely, high-level resistance, i.e. resistance to the highest drug concentration tested, was observed in 49% of the isolates, at rates between 2% (ethambutol) and 84% (rifampicin) according to the drug. Antituberculous drugs could be divided into three groups: predominantly high levels of resistance were observed for rifampicin, rifabutin, amikacin; low levels of resistance were mainly observed for ethambutol; and various levels of resistance were observed for isoniazid, streptomycin, capreomycin, *para*-aminosalicylic acid, ethionamide, ofloxacin and moxifloxacin.

Genotypic investigation of resistance

Data on the number of resistant strains in which we found at least one mutation involved in resistance are presented in Table 2. When molecular assays did not detect a mutation in a resistant strain, we repeated the molecular analysis on bacteria grown in the drug-containing tubes in order to avoid false test results due to heteroresistance, i.e. coexistence of susceptible and resistant bacteria.^{32,33} Genetic analysis was not done for *para*-aminosalicylic acid resistance since the underlying genetic mechanisms are still a matter of debate³⁴ and not for linezolid for which no resistant strains were observed. Overall, we observed resistance mutations in >80% of the resistant strains, except for ethambutol. Since the same mutation can confer cross-resistance, we also compared the phenotypes of isoniazid and ethionamide resistance in the case of *inhA* mutations, rifampicin and rifabutin resistance in the case of *rpoB* mutations, amikacin and capreomycin resistance in the case of a mutation in the *rrs* 1400 region and ofloxacin and moxifloxacin resistance in the case of *gyrA* mutations.

katG mutations were the most prevalent mutation (85%) in strains resistant to isoniazid, with S315T being the most frequent *katG* mutation (96%) and associated with an intermediate level of resistance (for the frequency of genotypes see Table 2, for genotype–phenotype relationships see Table 3 and for mutations in strains with low-level resistance see Table 4). Mutations in the *inhA* promoter region were associated with low-level isoniazid resistance. *rpoB* mutations at position 531 were the most

prevalent rifampicin resistance mutation (98/139, 71%) and were associated with high-level resistance to rifampicin and rifabutin. Altogether, 21 patterns of *rpoB* mutations were observed at 13 different codons, reflecting the diversity of the MDR strains in the nine European countries. We confirmed that *rpoB* mutations occurred also frequently at position 516 (12 strains) and at position 526 (14 strains). Mutations at position 526 were mostly

associated with high-level resistance to rifampicin and rifabutin (11/14 for rifampicin and 9/11 for rifabutin). In contrast, mutations at position 516 were mostly associated with low-level resistance to rifabutin (8/10 resistant strains) or even no resistance (1/11 strains tested). Some, but not all, mutations are shown in Table 3. Resistance to ethionamide was associated with mutations in *inhA* (55%), in *ethA* (61%) or both (16%). Mutations in

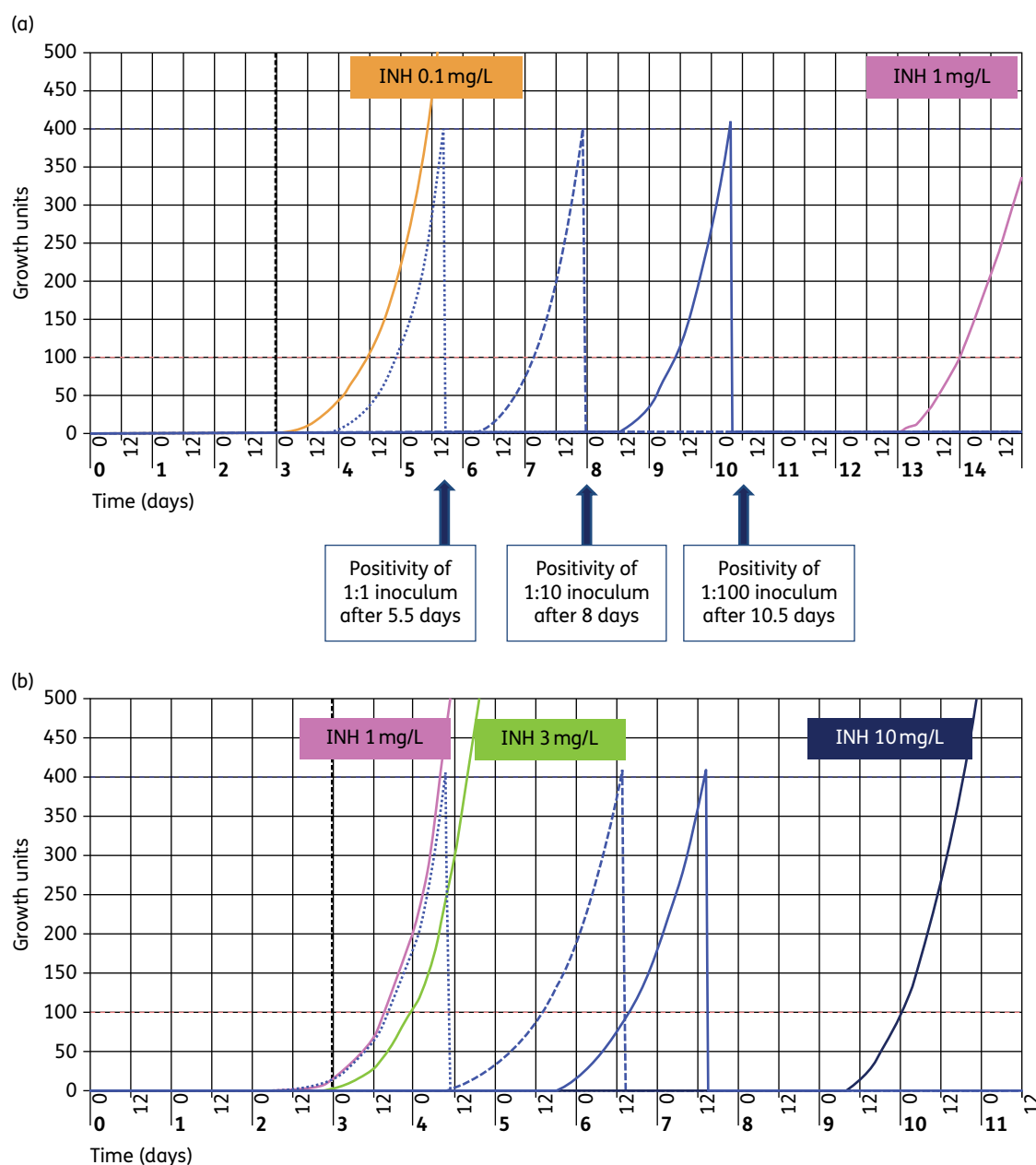


Figure 1. Representative results for quantitative resistance testing using the TB eXiST software. Growth in control tubes appears as blue lines; dotted line for 1:1; discontinuous line for 1:10 and continuous line for 1:100 (GC). (a) Low-level resistance to isoniazid (*inhA* c-15T): resistance to isoniazid at 0.1 mg/L (orange line) observed for 100% of the inoculum, but susceptibility at 1 mg/L (pink line). (b) Intermediate resistance to isoniazid (*katG* S315T): resistance to isoniazid observed at 1 mg/L (pink line) and at 3 mg/L (green line) for 100% of the inoculum, but susceptibility at 10 mg/L (dark blue line). (c) Homogeneous high-level resistance to ofloxacin (mutation *gyrA* D94A): resistance observed at 1 mg/L (pink line), 2 mg/L (green line) and 10 mg/L (dark blue line). (d) Heteroresistance for ofloxacin and intermediate level of resistance (*gyrA* A90V): resistance observed at 1 mg/L (pink line) and 2 mg/L (green line) for between 10% and 1% of the inoculum. See the text for interpretation of positive and negative growth results. INH, isoniazid; OFX, ofloxacin.

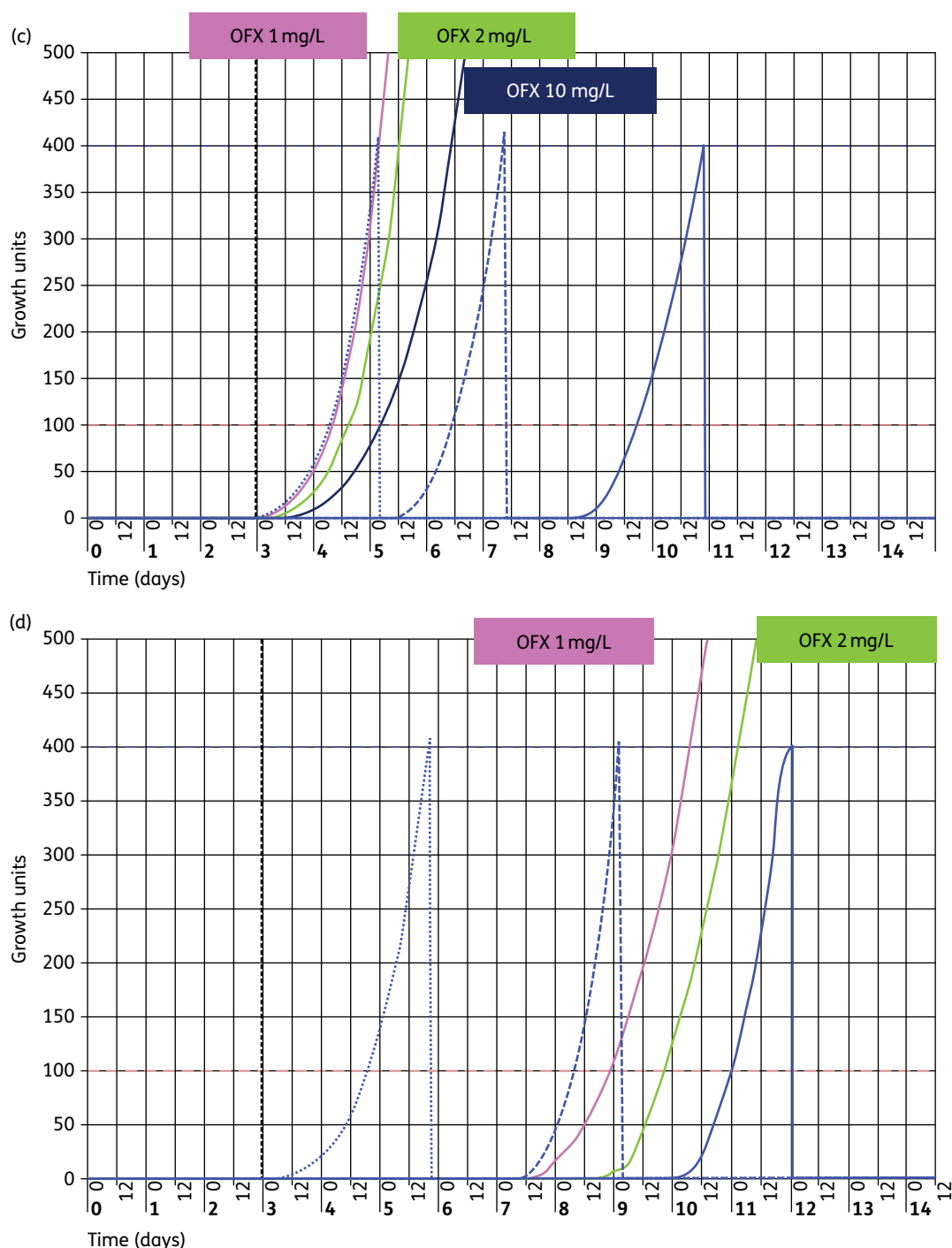


Figure 1. Continued

ethA were various with deletions and stop codons introduced at different sites of the gene sequence.

Phenotypic resistance to pyrazinamide, i.e. growth at the concentration of 100 mg/L, was highly associated with mutations in *pncA*: various missense mutations for 53 strains, deletion mutations for 4 strains and insertion mutations for 7 strains. In addition, pyrazinamidase production was negative in 31/33 (94%) resistant strains subjected to this biochemical test. This shows

that both altered *pncA* gene and absence of pyrazinamidase production confirmed the resistant character. *embB* mutations at the hot-spot 306 codon were observed in 70% of the resistant strains, indicating either that the remaining strains harbour an unknown mechanism of resistance or that the screening concentration does not reliably discriminate between susceptible and resistant strains. However, most of the strains devoid of *embB* mutations showed only a low level of resistance. We noticed that mutations

Table 1. Phenotypic resistance observed for the 139 MDR strains of *M. tuberculosis* and detailed for the level of resistance (except pyrazinamide) by quantitative DST

| Drug (list of concentrations tested in mg/L) | No. of resistant strains ^a | Low-level resistance ^b | Intermediate-level resistance ^c | High-level resistance ^d |
|--|---------------------------------------|-----------------------------------|--|------------------------------------|
| Isoniazid (0.1 , 1, 3, 10) | 139 | 11 (8%) | 109 (78%) | 19 (14%) |
| Rifampicin (1 , 4, 20) | 139 | 7 (5%) | 15 (11%) | 117 (84%) |
| Rifabutin (0.1 , 0.4, 2) | 118 | 11 (9%) | 23 (19%) | 84 (71%) |
| Ethambutol (5 , 12.5, 50) | 56 | 41 (73%) | 14 (25%) | 1 (2%) |
| PAS (4 , 16, 64) | 11 | 4 (36%) | 3 (27%) | 4 (36%) |
| Pyrazinamide (100) | 65 | NT | NT | NT |
| Streptomycin (1 , 4, 20) | 107 | 17 (16%) | 22 (21%) | 68 (64%) |
| Ethionamide (5 , 10, 25) | 57 | 10 (18%) | 10 (18%) | 37 (65%) |
| Amikacin (1 , 4, 20) | 22 | 4 (18%) | 0 | 18 (82%) |
| Capreomycin (2.5 , 5, 25) | 24 | 4 (17%) | 20 (83%) | 0 |
| Ofloxacin (1 , 2, 10) | 25 | 3 (12%) | 19 (76%) | 3 (12%) |
| Moxifloxacin (0.25 , 0.5, 2.5, 7.5) | 22 | 3 (14%) | 18 (82%) | 1 (5%) |
| Linezolid (1 , 4, 16) | 0 | 0 | 0 | 0 |
| Total resistant characters | 720 | 115 (16%) | 253 (35%) | 352 (49%) |

PAS, *para*-aminosalicylic acid; NT, not tested.

^aPhenotypic resistance was determined by growth at the screening concentration (in bold). This concentration was repeated in the quantitative DST along with higher concentrations of the drug.

^bLow-level resistance was defined as resistance at the screening concentration, but susceptibility at the intermediate drug concentration.

^cIntermediate-level resistance was defined as resistance at the screening concentration and the intermediate concentration, but susceptibility at the highest concentration.

^dHigh-level resistance was defined as resistance at all concentrations tested.

M306V and M306I were not associated with the same level of resistance to ethambutol: 42% (10/24) of the strains harbouring the mutation M306V were resistant at 12.5 mg/L, but only 7% (1/14) of those with the mutation M306I.

Resistance to streptomycin was associated either with a mutation in the *rrs* 530 region or in the *rpsL* gene encoding the S12 ribosomal protein (position 43 or 88, numbering system of *Escherichia coli*). For 23 streptomycin-resistant strains without *rrs* or *rpsL* mutations, we found a *gidB* mutation in 16 strains. This was more often associated with low-level resistance. For amikacin resistance, we observed the mutation a1408g in the *rrs* gene in all but four resistant strains, the latter showing resistance at a low level only. Capreomycin resistance was observed as cross-resistance with amikacin mediated by the *rrs* a1408g mutation and also as isolated capreomycin resistance with mutation in *tlyA* in five strains with no *rrs* mutation.

Resistance to fluoroquinolones correlated with *gyrA* mutations. However, the correlation was stronger for moxifloxacin than for ofloxacin, since three strains without *gyrA* and *gyrB* mutations showed a low level of resistance to ofloxacin, but susceptibility to moxifloxacin. The main problem for fluoroquinolone molecular resistance detection was heteroresistance, since in 72% (18/25) the *gyrA* mutation was evidenced only when molecular retesting was done on bacteria grown in drug-containing medium.

Discussion

The lack of standardization and reproducibility in DST of *M. tuberculosis* hinders the control of TB disease and facilitates the spread of drug-resistant organisms. This is especially true for second-line agents. In this multicentre study, we evaluated the feasibility and reliability of a standardized and automated DST procedure able to

quantify levels of drug resistance to first- and second-line antituberculous drugs. The results of our DST measurements were validated by assessing the concordance with resistance-associated gene mutations.

The primary objective of DST is to distinguish resistant strains from susceptible strains, since resistance is prognostic of treatment failure and relapse.³⁵ Historically, two principles were followed in DST: critical drug concentration and critical proportion.^{13,36,37} Several DST methods, including newly developed ones such as microscopic observation drug susceptibility, nitrate reductase assay and colorimetric tests, have since been described, all based on, but also limited by the principles of, critical proportion and critical drug concentration.^{17,18,38} Unfortunately, DST is done differently not only in different parts of the world, but even within Europe. In Europe alone, three methods are mainly used for DST of *M. tuberculosis*: proportion testing, the absolute concentration method and the resistance ratio. As a result of the different methods used, it is difficult to compare the results from one laboratory with those from another laboratory, even for the same patient and the same strain. In addition, for most drugs and techniques, only a single drug concentration is tested while the quantitative levels of resistance may be important for treatment.

We aimed to improve DST for MDR *M. tuberculosis* by increasing the accuracy of resistance detection as well as that of susceptibility assessment. Since exhaustive testing is required for MDR-TB cases, we invested into a DST technique compatible with automation, standardization and rapid time to result. Automated procedures offer significant advantages in terms of personnel handling, standardization and quality control.

The DST procedure we developed follows a first step in which bacterial growth is assessed in the presence of a 'screening drug

Table 2. Phenotypic and genotypic resistance per antituberculous drug among the 139 MDR strains of *M. tuberculosis* tested

| Drug | Phenotypic resistance ^a | | Genotypic resistance | | Gene and codon screened (no. of strains with mutation ^b ; % ^c) |
|--------------|------------------------------------|------------------------|--|---|--|
| | no. of resistant strains | resistance rate (%) | no. of strains with at least one mutation | rate of phenotypically resistant strains with mutation (%) | |
| Rifampicin | 139 | 100 | 139 | 100 | <i>rpoB</i> codons 511–533 ^d (139; 100) |
| Rifabutin | 118 | 100 | 118 | 100 | <i>rpoB</i> codons 511–533 ^d (118; 100) |
| Isoniazid | 139 | 100 | 135 | 97 | <i>katG</i> codon 315 ^e and others (115; 85) |
| Ethionamide | 57 | 46 | 49 | 86 | <i>inhA</i> promoter (30; 22) <i>inhA</i> gene ^f (15; 11) <i>ethA</i> (30; 61) <i>inhA</i> promoter and <i>inhA</i> gene ^{f,g} (27; 55) <i>ethR</i> (0; 0) |
| Ethambutol | 56 | 40 | 39 | 70 | <i>embB</i> codon 306 ^e (39; 100) |
| Pyrazinamide | 65 | 47 | 64 | 98 | <i>pncA</i> (64; 100%) |
| Streptomycin | 107 | 77 | 98 | 92 | <i>rpsL</i> codons 43–88 ^d (68; 69) <i>rrs</i> region 530 ^d (17; 17) <i>gidB</i> ^h (16; 16) |
| Amikacin | 22 | 16 | 18 | 82 | <i>rrs</i> region 1400 ^d –1495 (18; 100) |
| Capreomycin | 24 | 17 | 23 | 96 | <i>rrs</i> region 1400 ^d –1495 (18; 78) <i>tlyA</i> ⁱ (5; 22) |
| Ofloxacin | 25 | 18 | 22 | 88 | <i>gyrA</i> codons 88 ^e –94 (22; 100) <i>gyrB</i> ^j (0; 0) |
| Moxifloxacin | 22 | 16 | 22 | 100 | <i>gyrA</i> codons 88 ^e –94 (22; 100) <i>gyrB</i> ^j (0; 0) |
| PAS | 11 | 9 | NA | NA | NA |
| Linezolid | 0 | 0 | 0 | 0 | NA |

PAS, *para*-aminosalicylic acid; NA, not applicable (for PAS resistance, gene mutations have not been established; for linezolid, no resistant strains were observed).

^aPhenotypic resistance at the screening concentration.

^bStrains may have mutations in several genes (see the text for details).

^cPercentage of strains with mutation at this codon or in this gene.

^dNumbering system of *E. coli*.

^eNumbering system of *M. tuberculosis*.

^fSequence of the structural *inhA* gene.

^gSixty-seven out of 139 were studied for the entire *inhA* gene sequence.

^h*gidB* was sequenced for 18 of the 23 streptomycin-resistant strains without mutation in both *rrs* and *rpsL*.

ⁱ*tlyA* was sequenced for the six capreomycin-resistant strains without mutation in *rrs*.

^j*gyrB* was sequenced in eight ofloxacin-resistant strains among which three strains were without mutation in *gyrA*.

concentration' that is close to the ECOFF described recently for isoniazid, rifampicin, ethambutol and fluoroquinolones.^{29–31} This concentration is the smallest MIC value for the WT strains, i.e. susceptible strains will not grow at this concentration. The second step was limited to strains resistant at the screening drug concentration. This second step confirmed the resistance by retesting the screening concentration and in addition provided a quantitative assessment of resistance by testing different drug concentrations. Knowing the level of resistance has two advantages: it gives information on the putative mechanism of resistance and it may have a significant clinical impact. Recent studies showed that an increase in the dosage of isoniazid or rifampicin may improve MDR outcome.^{39,40} A low level of resistance can also be overcome by the use of a more potent drug such as the use of moxifloxacin instead of ofloxacin in case of defined *gyrA* mutations.^{41,42} We

also confirmed that some strains resistant to rifampicin are only low-level resistant to rifabutin and harboured a specific *rpoB* mutation at codon 516.^{43,44} Although the clinical efficacy of rifabutin in these cases remains to be demonstrated, the lack of effective drugs in some MDR cases may benefit from rifabutin if still active. A low level of resistance to ethionamide, as we observed in the majority of strains, may allow the use of an ethionamide booster in the future.^{45,46}

In addition to quantitative DST determination, we also searched for resistance-associated mutations with the view to confirm that most of the strains categorized as resistant were not WT strains and to increase our knowledge on the resistance levels these mutations confer. Hot-spot mutations were found as expected in *rpoB* at codon 531 for strains resistant to rifampicin, in *katG* at codon 315 for strains resistant to isoniazid, in *gyrA* at codon 90 or 94 for strains

Table 3. Genotype–phenotype relationship of the most prevalent resistance gene mutations

| Drug | Mutation ^a | Low-level resistance ^b | Intermediate-level resistance ^c | High-level resistance ^d |
|--------------|----------------------------------|-----------------------------------|--|------------------------------------|
| Isoniazid | <i>katG</i> S315T (n=99) | 1/99 | 92/99 | 6/99 |
| | <i>inhA</i> promoter (n=6) | 5/6 | 1/6 | 0/6 |
| Rifampicin | <i>rpoB</i> S531L (n=98) | 1/98 | 2/98 | 95/98 |
| | <i>rpoB</i> D516V (n=12) | 2/12 | 9/12 | 1/12 |
| | <i>rpoB</i> H526L (n=3) | 2/3 | 0/3 | 1/3 |
| | <i>rpoB</i> H526Y (n=4) | 0/4 | 1/4 | 3/4 |
| | <i>rpoB</i> H526D (n=6) | 0/6 | 0/6 | 6/6 |
| Rifabutin | <i>rpoB</i> S531L (n=87) | 0/87 | 17/87 | 70/87 |
| | <i>rpoB</i> D516V (n=9) | 6/9 | 2/9 | 1/9 |
| | <i>rpoB</i> H526L (n=2) | 1/2 | 0/2 | 1/2 |
| | <i>rpoB</i> H526Y (n=3) | 0/3 | 0/3 | 3/3 |
| | <i>rpoB</i> H526D (n=5) | 0/5 | 0/5 | 5/5 |
| Ethambutol | <i>embB</i> M306I (n=14) | 13/14 | 1/14 | 0/14 |
| | <i>embB</i> M306V (n=24) | 14/24 | 10/24 | 0/24 |
| Ethionamide | <i>inhA</i> promoter (n=8) | 2/8 | 2/8 | 4/8 |
| | <i>ethA</i> (n=21) | 4/21 | 3/21 | 14/21 |
| Streptomycin | <i>rrs</i> a523c (n=7) | 0/7 | 2/7 | 5/7 |
| | <i>rrs</i> c526t (n=8) | 3/8 | 4/8 | 1/8 |
| | <i>rpsL</i> K43R (n=55) | 0/55 | 2/55 | 53/55 |
| | <i>rpsL</i> K88R (n=9) | 0/9 | 5/9 | 4/9 |
| | <i>gidB</i> ^e (n=16) | 9/16 | 7/16 | 0/16 |
| Amikacin | <i>rrs</i> a1408 mutation (n=18) | 0/18 | 0/18 | 18/18 |
| | <i>rrs</i> a1408 WT (n=4) | 4/4 | 0/4 | 0/4 |
| Capreomycin | <i>rrs</i> a1408 mutation (n=18) | 3/18 | 15/18 | 0/18 |
| | <i>tlyA</i> ^f (n=5) | 1/5 | 4/5 | 0/5 |
| Ofloxacin | <i>gyrA</i> A90V (n=3) | 0/3 | 3/3 | 0/3 |
| | <i>gyrA</i> S91P (n=5) | 0/5 | 5/5 | 0/5 |
| | <i>gyrA</i> D94G (n=7) | 0/7 | 6/7 | 1/7 |
| Moxifloxacin | <i>gyrA</i> A90V (n=3) | 2/3 | 1/3 | 0/3 |
| | <i>gyrA</i> S91P (n=5) | 0/5 | 4/5 | 1/5 |
| | <i>gyrA</i> D94G (n=7) | 0/7 | 7/7 | 0/7 |

^aOnly single mutations were considered and mutations observed in less than three strains are not shown.

^bLow-level resistance was defined as resistance at the screening concentration, but susceptibility at the intermediate drug concentration.

^cIntermediate-level resistance was defined as resistance at the screening concentration and the intermediate concentration, but susceptibility at the highest concentration.

^dHigh-level resistance was defined as resistance at all concentrations tested.

^eEighteen out of 23 streptomycin-resistant strains with no mutation in *rrs* and *rpsL* were tested for *gidB*.

^fThe six capreomycin-resistant strains WT for *rrs* 1400 were tested for *tlyA*.

resistant to ofloxacin and moxifloxacin, in *rpsL* at codons 43 and 88 for strains resistant to streptomycin and in *rrs* at nucleotide a1408 for strains resistant to amikacin. Resistance mutations were scattered in genes coding for *ethA* and *pncA* as described previously, since many different mutations can confer a loss or decrease in the function of these proteins, which activate ethionamide and pyrazinamide, respectively.^{47,48} Although some of the latter mutations have not been described yet, we consider it unlikely that they are related to simple gene polymorphisms.

To date, evidence is accumulating that the term ‘resistance’ in *M. tuberculosis* is not a biological entity, but quite heterogeneous and composed of quantitatively different levels of drug resistance. Most significantly, the quantitatively different resistance levels—low, moderate and high levels of resistance—are associated with different genetic mutations.^{31,49} This biological diversity of

resistance is not recognized by the current critical concentration or ECOFF testing, but requires measures of quantitative resistance determination. Through this multicentre study, we established and evaluated a standardized protocol for quantitative DST. The procedure developed integrates the established principles of critical concentration and critical proportion, combined with quantitative measures of drug resistance, automated detection and continuous monitoring, exploring drug susceptibility in the dimensions of concentration, proportion and time. Work still needs to be done to resolve some discrepancies between phenotypic and genotypic tests as in the case of ethambutol. In addition, group 4 and 5 antituberculous drugs⁸ and new ones, such as bedaquiline and delamanid, will need to be tested.^{50,51} Hopefully, a more thorough description of resistance in clinical strains will allow better exploitation of available antituberculous agents in the treatment

Table 4. Genotypic resistance detailed for the *M. tuberculosis* strains with a low level of resistance

| Resistance phenotype (antibiotic concentration in mg/L) | No. of strains with low-level resistance | Mutations (no. of strains per genotype) ^a |
|---|--|--|
| R to INH (0.1), S to (1) | 11 | <i>inhA</i> promoter: c–15t (5), t–8c (1) <i>katG</i> : S315T (1), T149C (1) WT for <i>katG</i> and <i>inhA</i> (3) |
| R to RIF (1), S to (4) | 7 | <i>rpoB</i> : D516V (2), delN519 (1), H526L (2), S531L (1), L533P+N518D (1) |
| R to RFB (0.1), S to (0.4) | 11 | <i>rpoB</i> : L511P+D516G (1), D516V (6), D516Y (1), delN519 (1), S522L (1), H526L (1) |
| R to EMB (5), S to (12.5) | 41 | <i>embB</i> : M306V (14), M306I (13), D328G+G406A (1), WT (13) |
| R to STR (1), S to (4) | 17 | <i>rpsL</i> : WT (17) <i>rrs</i> : c523g (1), c526t (3), WT (13) <i>gidB</i> ^b : L16R+G73R (1), E40D (1), G69D (1), L74stop (1), L79W (1), A80P (1), S100F (1), A139V (1), deletion (1), WT (1) |
| R to ETH (5), S to (10) | 10 | <i>inhA</i> promoter: t–8c (1), c–15t (1), WT (8) <i>ethA</i> : M1R (1), I105L (1), deletion (2), WT (6) |
| R to AMK (1), S to (4) | 4 | <i>rrs</i> : WT (4) |
| R to CAP (2.5), S to (5) | 4 | <i>rrs</i> : a1408g (3) <i>tlyA</i> : V64G (1) |
| R to OFX (1), S (2) | 3 | <i>gyrA</i> : WT (3) |
| R to MXF (0.25), S (0.5) | 3 | <i>gyrA</i> : D89N (1), A90V (2) |

INH, isoniazid; RIF, rifampicin; RFB, rifabutin; EMB, ethambutol; ETH, ethionamide; STR, streptomycin; AMK, amikacin; CAP, capreomycin; OFX, ofloxacin; MXF, moxifloxacin; R, resistant; S, susceptible.

^aOnly single mutations are listed, unless indicated otherwise. See Table 2 for numbering systems.

^b*gidB* was tested for 10 of the 17 low-level streptomycin-resistant strains.

of drug-resistant TB disease, by tailoring therapy according to the resistance characteristics of individual strains. The time has come for personalized medicine in the treatment of drug-resistant TB disease.

Acknowledgements

We thank very much the following colleagues for their help in the study design, strain collection and testing: Gema Barbeito, Isabel Couto, Bárbara Gomila, Vincent Jarlier, Pontus Jureen, Paola Mantegani, Maryse Fauville-Dufaux, Faiza Mougari, Jorge Ramos, Karine Soetaert, Nicolas Veziris and Jim Werngren. We thank the technicians involved in each laboratory participating in the study. We are grateful to Ulrike Kunert for secretarial and logistical assistance.

Funding

This study was supported by internal funding.

Transparency declarations

BD provided assistance for software and helped organizing meetings of the network. BD had no influence on the design of the study or on the decision to publish. E. C. B. is a consultant of BD. All other authors: none to declare.

Supplementary data

Table S1 is available as Supplementary data at JAC Online (<http://jac.oxfordjournals.org/>).

References

- Gandhi NR, Nunn P, Dheda K *et al.* Multidrug-resistant and extensively drug-resistant tuberculosis: a threat to global control of tuberculosis. *Lancet* 2010; **375**: 1830–43.
- ECDC/WHO Regional Office for Europe. *Tuberculosis Surveillance and Monitoring in Europe* 2014. Stockholm: ECDC, 2014.
- Dheda K, Gumbo T, Gandhi NR *et al.* Global control of tuberculosis: from extensively drug-resistant to untreatable tuberculosis. *Lancet Respir Med* 2013; **2**: 321–38.
- Espinal MA, Kim SJ, Suarez PG *et al.* Standard short-course chemotherapy for drug-resistant tuberculosis: treatment outcomes in 6 countries. *JAMA* 2000; **283**: 2537–45.
- Quy HT, Lan NT, Borgdorff MW *et al.* Drug resistance among failure and relapse cases of tuberculosis: is the standard re-treatment regimen adequate? *Int J Tuberc Lung Dis* 2003; **7**: 631–6.
- Burman WJ. The value of in vitro drug activity and pharmacokinetics in predicting the effectiveness of antimycobacterial therapy: a critical review. *Am J Med Sci* 1997; **313**: 355–63.
- Pietersen E, Ignatius E, Streicher EM *et al.* Long-term outcomes of patients with extensively drug-resistant tuberculosis in South Africa: a cohort study. *Lancet* 2014; **383**: 1230–9.
- WHO. *Guidelines for the Programmatic Management of Multidrug Resistant Tuberculosis*. Geneva: WHO, 2011.
- Flament-Saillour M, Robert J, Jarlier V *et al.* Outcome of multi-drug-resistant tuberculosis in France: a nationwide case-control study. *Am J Respir Crit Care Med* 1999; **160**: 587–93.
- Drobniewski F, Eltringham I, Graham C *et al.* A national study of clinical and laboratory factors affecting the survival of patients with multiple drug resistant tuberculosis in the UK. *Thorax* 2002; **57**: 810–6.

- 11 Turett GS, Telzak EE, Torian LV et al. Improved outcomes for patients with multidrug-resistant tuberculosis. *Clin Infect Dis* 1995; **21**: 1238–44.
- 12 Johnston JC, Shahidi NC, Sadatsafavi M et al. Treatment outcomes of multidrug-resistant tuberculosis: a systematic review and meta-analysis. *PLoS One* 2009; **4**: e6914.
- 13 Heifets LB, Cangelosi GA. Drug susceptibility testing of *Mycobacterium tuberculosis*: a neglected problem at the turn of the century. *Int J Tuberc Lung Dis* 1999; **3**: 564–81.
- 14 Cambau E, Rush-Gerdes S. First and second line susceptibility testing for *Mycobacterium tuberculosis* complex. In: ECDC, ed. *Mastering the Basics of Tuberculosis Control: Development of a Handbook on TB Diagnostic Methods*. Stockholm: ECDC, 2011; 79–87.
- 15 Drobniewski F, Rusch-Gerdes S, Hoffner S. Antimicrobial susceptibility testing of *Mycobacterium tuberculosis* (EUCAST document E.DEF 8.1)—report of the Subcommittee on Antimicrobial Susceptibility Testing of *Mycobacterium tuberculosis* of the European Committee for Antimicrobial Susceptibility Testing (EUCAST) of the European Society of Clinical Microbiology and Infectious Diseases (ESCMID). *Clin Microbiol Infect* 2007; **13**: 1144–56.
- 16 Streicher EM, Muller B, Chihota V et al. Emergence and treatment of multidrug resistant (MDR) and extensively drug-resistant (XDR) tuberculosis in South Africa. *Infect Genet Evol* 2011; **12**: 686–94.
- 17 Martin A, Imperiale B, Ravolonandriana P et al. Prospective multicentre evaluation of the direct nitrate reductase assay for the rapid detection of extensively drug-resistant tuberculosis. *J Antimicrob Chemother* 2014; **69**: 441–4.
- 18 Fitzwater SP, Sechler GA, Jave O et al. Second-line anti-tuberculosis drug concentrations for susceptibility testing in the MODS assay. *Eur Respir J* 2012; **41**: 1163–71.
- 19 Clinical and Laboratory Standards Institute. *Susceptibility Testing of Mycobacteria, Nocardiae, and Other Aerobic Actinomycetes—Second Edition: Approved Standard M24-A2*. CLSI, Wayne, PA, USA, 2011.
- 20 Bernard C, Brossier F, Sougakoff W et al. A surge of MDR and XDR tuberculosis in France among patients born in the former Soviet Union. *Euro Surveill* 2013; **18**: pii=20555.
- 21 Perdigao J, Macedo R, Silva C et al. From multidrug-resistant to extensively drug-resistant tuberculosis in Lisbon, Portugal: the stepwise mode of resistance acquisition. *J Antimicrob Chemother* 2012; **68**: 27–33.
- 22 Cambau E, Truffot-Pernot C, Boulahbal F et al. Mycobacterial growth indicator tube versus the proportion method on Lowenstein–Jensen medium for antibiotic susceptibility testing of *Mycobacterium tuberculosis*. *Eur J Clin Microbiol Infect Dis* 2000; **19**: 938–42.
- 23 Hillemann D, Rusch-Gerdes S, Richter E. Evaluation of the GenoType MTBDRplus assay for rifampin and isoniazid susceptibility testing of *Mycobacterium tuberculosis* strains and clinical specimens. *J Clin Microbiol* 2007; **45**: 2635–40.
- 24 Brossier F, Veziris N, Aubry A et al. Detection by GenoType MTBDRsl test of complex mechanisms of resistance to second-line drugs and ethambutol in multidrug-resistant *Mycobacterium tuberculosis* complex isolates. *J Clin Microbiol* 2010; **48**: 1683–9.
- 25 Ritter C, Lucke K, Sirgel FA et al. Evaluation of the AID TB resistance line probe assay for rapid detection of genetic alterations associated with drug resistance in *Mycobacterium tuberculosis* strains. *J Clin Microbiol* 2014; **52**: 940–6.
- 26 Bemer P, Palicova F, Rusch-Gerdes S et al. Multicenter evaluation of fully automated BACTEC Mycobacteria Growth Indicator Tube 960 system for susceptibility testing of *Mycobacterium tuberculosis*. *J Clin Microbiol* 2002; **40**: 150–4.
- 27 Rodrigues C, Jani J, Shenai S et al. Drug susceptibility testing of *Mycobacterium tuberculosis* against second-line drugs using the Bactec MGIT 960 System. *Int J Tuberc Lung Dis* 2008; **12**: 1449–55.
- 28 Springer B, Lucke K, Calligaris-Maibach R et al. Quantitative drug susceptibility testing of *Mycobacterium tuberculosis* by use of MGIT 960 and EpiCenter instrumentation. *J Clin Microbiol* 2009; **47**: 1773–80.
- 29 Schon T, Jureen P, Chrysanthou E et al. Wild-type distributions of seven oral second-line drugs against *Mycobacterium tuberculosis*. *Int J Tuberc Lung Dis* 2011; **15**: 502–9.
- 30 Angeby KA, Jureen P, Giske CG et al. Wild-type MIC distributions of four fluoroquinolones active against *Mycobacterium tuberculosis* in relation to current critical concentrations and available pharmacokinetic and pharmacodynamic data. *J Antimicrob Chemother* 2010; **65**: 946–52.
- 31 Bottger EC. The ins and outs of *Mycobacterium tuberculosis* drug susceptibility testing. *Clin Microbiol Infect* 2011; **17**: 1128–34.
- 32 Folkvardsen DB, Svensson E, Thomsen VO et al. Can molecular methods detect 1% isoniazid resistance in *Mycobacterium tuberculosis*? *J Clin Microbiol* 2013; **51**: 1596–9.
- 33 Streicher EM, Bergval I, Dheda K et al. *Mycobacterium tuberculosis* population structure determines the outcome of genetics-based second-line drug resistance testing. *Antimicrob Agents Chemother* 2012; **56**: 2420–7.
- 34 Mathys V, Wintjens R, Lefevre P et al. Molecular genetics of para-aminosalicylic acid resistance in clinical isolates and spontaneous mutants of *Mycobacterium tuberculosis*. *Antimicrob Agents Chemother* 2009; **53**: 2100–9.
- 35 Canetti G. Present aspects of bacterial resistance in tuberculosis. *Am Rev Respir Dis* 1965; **92**: 687–703.
- 36 Canetti G, Froman S, Grosset J et al. *Mycobacteria: Laboratory Methods for Testing Drug Sensitivity and Resistance*. Bull World Health Organ 1963; **29**: 565–78.
- 37 Mitchison DA. What is drug resistance? *Tubercle* 1969; **50**: Suppl: 44–7.
- 38 Banfi E, Scialino G, Monti-Bragadin C. Development of a microdilution method to evaluate *Mycobacterium tuberculosis* drug susceptibility. *J Antimicrob Chemother* 2003; **52**: 796–800.
- 39 Katiyar SK, Bihari S, Prakash S et al. A randomised controlled trial of high-dose isoniazid adjuvant therapy for multidrug-resistant tuberculosis. *Int J Tuberc Lung Dis* 2008; **12**: 139–45.
- 40 van Ingen J, Aarnoutse R, de Vries G et al. Low-level rifampicin-resistant *Mycobacterium tuberculosis* strains raise a new therapeutic challenge. *Int J Tuberc Lung Dis* 2011; **15**: 990–2.
- 41 Maruri F, Sterling TR, Kaiga AW et al. A systematic review of gyrase mutations associated with fluoroquinolone-resistant *Mycobacterium tuberculosis* and a proposed gyrase numbering system. *J Antimicrob Chemother* 2012; **67**: 819–31.
- 42 Fillion A, Aubry A, Brossier F et al. Impact of fluoroquinolone resistance on bactericidal and sterilizing activity of a moxifloxacin-containing regimen in murine tuberculosis. *Antimicrob Agents Chemother* 2013; **57**: 4496–500.
- 43 Yang B, Koga H, Ohno H et al. Relationship between antimycobacterial activities of rifampicin, rifabutin and KRM-1648 and rpoB mutations of *Mycobacterium tuberculosis*. *J Antimicrob Chemother* 1998; **42**: 621–8.
- 44 Sirgel FA, Warren RM, Bottger EC et al. The rationale for using rifabutin in the treatment of MDR and XDR tuberculosis outbreaks. *PLoS One* 2013; **8**: e59414.
- 45 Grau T, Selchow P, Tigges M et al. Phenylethyl butyrate enhances the potency of second-line drugs against clinical isolates of *Mycobacterium tuberculosis*. *Antimicrob Agents Chemother* 2012; **56**: 1142–5.
- 46 Willand N, Dirie B, Carette X et al. Synthetic EthR inhibitors boost anti-tuberculous activity of ethionamide. *Nat Med* 2009; **15**: 537–44.

- 47** Petrella S, Gelus-Ziental N, Maudry A et al. Crystal structure of the pyrazinamidase of *Mycobacterium tuberculosis*: insights into natural and acquired resistance to pyrazinamide. *PLoS One* 2011; **6**: e15785.
- 48** Brossier F, Veziris N, Truffot-Pernot C et al. Molecular investigation of resistance to the antituberculous drug ethionamide in multidrug-resistant clinical isolates of *Mycobacterium tuberculosis*. *Antimicrob Agents Chemother* 2010; **55**: 355–60.
- 49** Springer B, Calligaris-Maibach RC, Ritter C et al. Tuberculosis drug resistance in an area of low endemicity in 2004 to 2006: semiquantitative drug susceptibility testing and genotyping. *J Clin Microbiol* 2008; **46**: 4064–7.
- 50** Gler MT, Skripconoka V, Sanchez-Garavito E et al. Delamanid for multidrug-resistant pulmonary tuberculosis. *N Engl J Med* 2012; **366**: 2151–60.
- 51** Andries K, Verhasselt P, Guillemont J et al. A diarylquinoline drug active on the ATP synthase of *Mycobacterium tuberculosis*. *Science* 2005; **307**: 223–7.